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#3

SEQUENCE LISTING

<110> GORING, Daphne R. et al.

<120> PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

<130> P 25,762 USA

<140> US 10/069,304

<141> 2002-02-19

<150> PCT/CA00/00966

<151> 2000-08-18

<150> US 60/149,466

<151> 1999-08-19

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<151> 1999-10-13

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<170> PatentIn Ver. 2.1

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<400> 5

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Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu Gly Phe
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Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr Val His
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Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln Leu Lys
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Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val Glu Ile
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Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met Glu Trp
385 390 395 400

Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu Ser Tyr
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Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala Asp Phe
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Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser Thr Arg
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Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala Ser Gly
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Ser	Ser	Gly	Pro	Val	Val	Ser	Pro	Ser	Leu	Thr	Ser	Pro	Ser	Lys	Gly	
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gtc Val 385	tat Tyr	aaa Lys	ggt Gly	aca Thr	ttg Leu 390	cag Gln	gat Asp	ggt Gly	aaa Lys	gtt Val 395	gtt Val	gcg Ala	gtt Val	aag Lys	cag Gln 400	1200
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gag Glu	atc Ile	atc Ile	agc Ser 420	cgc Arg	gtt Val	cat His	cat His	cgc Arg 425	cat His	ttg Leu	gtc Val	tct Ser	ctg Leu 430	gtt Val	ggt Gly	1296
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aat	caa	acc	ttg	gag	cat	cat	ttg	cat	gag	tgg	tct	aag	aga	gtc	cgg	1392

Asn	Gln	Thr	Leu	Glu	His	His	Leu	His	Glu	Trp	Ser	Lys	Arg	Val	Arg	
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Ile	Ala	Ile	Gly	Ser	Ala	Lys	Gly	Leu	Ala	Tyr	Leu	His	Glu	Asp	Cys	
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His	Pro	Lys	Ile	Ile	His	Arg	Asp	Ile	Lys	Ser	Ala	Asn	Ile	Leu	Leu	
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Asp	Asp	Glu	Tyr	Glu	Ala	Gln	Ala	Ile	Met	Lys	Ser	Ser	Phe	Ser	Leu	
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Asn	Leu	Ser	Tyr	Asp	Cys	Lys	Val	Leu	Val	Ala	Asp	Phe	Gly	Leu	Ala	
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Cys	Asp	Gly	Asp	Ser	Gly	Asp	Ile	Ser	Asn	Gly	Ile	Lys	Ile	Gly	Gln	
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Arg	Lys	Met	Ala	Phe	Gly	Gly	Asp	Asn	Ser	Val	Glu	Ser	Gly	Leu	Tyr	
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<212> PRT

<213> Arabidopsis thaliana

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Pro His His Gln Met Gln Ser Ser Gly Thr Pro Asp Ser Ala Ile Leu				335
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Gly Ser Gly Gln Thr His Phe Ser Tyr Glu Glu Leu Ala Glu Ile Thr				350
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Gln Gly Phe Ala Arg Lys Asn Ile Leu Gly Glu Gly Gly Phe Gly Cys				365
		370		375
Val Tyr Lys Gly Thr Leu Gln Asp Gly Lys Val Val Ala Val Lys Gln				380
385		390		395
Leu Lys Ala Gly Ser Gly Gln Gly Asp Arg Glu Phe Lys Ala Glu Val				400
		405		410
Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly				415
		420		425
Tyr Cys Ile Ser Asp Gln His Arg Leu Leu Ile Tyr Glu Tyr Val Ser				430
		435		440
Asn Gln Thr Leu Glu His His Leu His Glu Trp Ser Lys Arg Val Arg				445
		450		455
Ile Ala Ile Gly Ser Ala Lys Gly Leu Ala Tyr Leu His Glu Asp Cys				460
465		470		475
His Pro Lys Ile Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu				480
		485		490
Asp Asp Glu Tyr Glu Ala Gln Ala Ile Met Lys Ser Ser Phe Ser Leu				495
		500		505
Asn Leu Ser Tyr Asp Cys Lys Val Leu Val Ala Asp Phe Gly Leu Ala				510
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Arg Leu Asn Asp Thr Thr Gln Thr His Val Ser Thr Arg Val Met Gly				525
		530		535
Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ser Ser Gly Lys Leu Thr				540
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Asp Arg Ser Asp Val Phe Ser Phe Gly Val Leu Leu Glu Leu Val				560
		565		570
Thr Gly Arg Lys Pro Val Asp Gln Thr Gln Pro Leu Gly Glu Glu Ser				575
		580		585
Leu Val Glu Trp Ala Arg Pro Leu Leu Leu Lys Ala Ile Glu Thr Gly				590
		595		600
Asp Leu Ser Glu Leu Ile Asp Thr Arg Leu Glu Lys Arg Tyr Val Glu				605
		610		615
His Glu Val Phe Arg Met Ile Glu Thr Ala Ala Ala Cys Val Arg His				620
625		630		635
Ser Gly Pro Lys Arg Pro Arg Met Val Gln Val Val Arg Ala Leu Asp				640
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Cys Asp Gly Asp Ser Gly Asp Ile Ser Asn Gly Ile Lys Ile Gly Gln				655
		660		665
Ser Thr Thr Tyr Asp Ser Gly Gln Tyr Asn Glu Asp Ile Met Lys Phe				670
		675		680
Arg Lys Met Ala Phe Gly Gly Asp Asn Ser Val Glu Ser Gly Leu Tyr				685
		690		695
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 Pro Ser Pro Pro Ser Asn Thr Asn Ser Thr Thr Ser Ser Pro Pro Ala
 20 25 30

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Pro	Pro	Pro	Asp	Ser	Thr	Ser	Pro	Pro	Ala	Pro	Gln	Ala	Pro	Asn	Pro	
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Gln	Tyr	Tyr	Gly	Asn	Asn	Asn	Asn	Asn	Asn	Ala	Ser	Gln	Asn	Tyr	Pro	
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495

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Pro Asp Ile Ser Ala Ser Phe Ser Pro Pro Pro Ala Pro Pro Thr Gln	
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Asn Pro Ser Pro Gln Thr Pro Glu Asn Pro Ser Pro Pro Ala Pro Glu	
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Gly Ser Thr Pro Val Thr Pro Pro Ala Pro Pro Gln Thr Pro Ser Asn	
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Gln Ser Pro Glu Arg Pro Thr Pro Pro Ser Pro Gly Ala Asn Asp Asp	
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Leu	Ser	Pro	Gly	Ser	Val	Ser	Ser	Glu	Tyr	Asp	Ala	Ser	Ser	Tyr	Thr	
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2025

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<213> Arabidopsis thaliana

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Gly	Ser	Thr	Pro	Val	Thr	Pro	Pro	Ala	Pro	Pro	Gln	Thr	Pro	Ser	Asn
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Phe	Leu	Pro	Ala	Lys	Pro	Ser	Pro	Pro	Pro	Ser	Ser	Pro	Pro	Ser	Glu
		115					120					125			
Thr	Val	Pro	Pro	Gly	Asn	Thr	Ile	Ser	Pro	Pro	Pro	Arg	Ser	Leu	Pro
		130				135					140				
Ser	Glu	Ser	Thr	Pro	Pro	Val	Asn	Thr	Ala	Ser	Pro	Pro	Pro	Pro	Ser
145					150					155					160
Pro	Pro	Arg	Arg	Arg	Ser	Gly	Pro	Lys	Pro	Ser	Phe	Pro	Pro	Pro	Ile
				165				170						175	
Asn	Ser	Ser	Pro	Pro	Asn	Pro	Ser	Pro	Asn	Thr	Pro	Ser	Leu	Pro	Glu
			180					185					190		
Thr	Ser	Pro	Pro	Pro	Lys	Pro	Pro	Leu	Ser	Thr	Thr	Pro	Phe	Pro	Ser
		195					200					205			
Ser	Ser	Thr	Pro	Pro	Pro	Lys	Lys	Ser	Pro	Ala	Ala	Val	Thr	Leu	Pro
		210				215					220				
Phe	Phe	Gly	Pro	Ala	Gly	Gln	Leu	Pro	Asp	Gly	Thr	Val	Ala	Pro	Pro
225					230					235					240
Ile	Gly	Pro	Val	Ile	Glu	Pro	Lys	Thr	Ser	Pro	Ala	Glu	Ser	Ile	Ser
				245				250						255	
Pro	Gly	Thr	Pro	Gln	Pro	Leu	Val	Pro	Lys	Ser	Leu	Pro	Val	Thr	Thr
			260					265					270		
Ser	Tyr	His	Arg	Ser	Ser	Ala	Gly	Phe	Leu	Phe	Gly	Gly	Val	Ile	Val
		275					280					285			
Gly	Ala	Leu	Leu	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Phe	Val	Phe	Tyr	Arg
		290				295					300				
Ala	Thr	Arg	Asn	Arg	Asn	Asn	Asn	Ser	Ser	Ser	Ala	His	His	Gln	Ser
305					310					315					320
Lys	Thr	Pro	Ser	Lys	Val	Gln	His	His	Arg	Gly	Gly	Asn	Ala	Gly	Thr
				325					330					335	
Asn	Gln	Ala	His	Val	Ile	Thr	Met	Pro	Pro	Pro	Ile	His	Ala	Lys	Tyr
			340					345					350		
Ile	Ser	Ser	Gly	Gly	Cys	Asp	Thr	Lys	Glu	Asn	Asn	Ser	Val	Ala	Lys
		355					360					365			
Asn	Ile	Ser	Met	Pro	Ser	Gly	Met	Phe	Ser	Tyr	Glu	Glu	Leu	Ser	Lys
		370				375					380				
Ala	Thr	Gly	Gly	Phe	Ser	Glu	Glu	Asn	Leu	Leu	Gly	Glu	Gly	Gly	Phe
385					390					395					400
Gly	Tyr	Val	His	Lys	Gly	Val	Leu	Lys	Asn	Gly	Thr	Glu	Val	Ala	Val
				405					410					415	
Lys	Gln	Leu	Lys	Ile	Gly	Ser	Tyr	Gln	Gly	Glu	Arg	Glu	Phe	Gln	Ala
			420					425					430		
Glu	Val	Asp	Thr	Ile	Ser	Arg	Val	His	His	Lys	His	Leu	Val	Ser	Leu
		435					440					445			
Val	Gly	Tyr	Cys	Val	Asn	Gly	Asp	Lys	Arg	Leu	Leu	Val	Tyr	Glu	Phe
		450				455					460				

Val	Pro	Lys	Asp	Thr	Leu	Glu	Phe	His	Leu	His	Glu	Asn	Arg	Gly	Ser
465					470					475					480
Val	Leu	Glu	Trp	Glu	Met	Arg	Leu	Arg	Ile	Ala	Val	Gly	Ala	Ala	Lys
				485					490						495
Gly	Leu	Ala	Tyr	Leu	His	Glu	Asp	Cys	Ser	Pro	Thr	Ile	Ile	His	Arg
			500					505						510	
Asp	Ile	Lys	Ala	Ala	Asn	Ile	Leu	Leu	Asp	Ser	Lys	Phe	Glu	Ala	Lys
		515					520					525			
Val	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Phe	Phe	Ser	Asp	Thr	Asn	Ser	Ser
	530					535					540				
Phe	Thr	His	Ile	Ser	Thr	Arg	Val	Val	Gly	Thr	Phe	Gly	Tyr	Met	Ala
545					550					555					560
Pro	Glu	Tyr	Ala	Ser	Ser	Gly	Lys	Val	Thr	Asp	Lys	Ser	Asp	Val	Tyr
				565					570					575	
Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Arg	Pro	Ser	Ile
			580					585					590		
Phe	Ala	Lys	Asp	Ser	Ser	Thr	Asn	Gln	Ser	Leu	Val	Asp	Trp	Ala	Arg
		595					600					605			
Pro	Leu	Leu	Thr	Lys	Ala	Ile	Ser	Gly	Glu	Ser	Phe	Asp	Phe	Leu	Val
	610					615					620				
Asp	Ser	Arg	Leu	Glu	Lys	Asn	Tyr	Asp	Thr	Thr	Gln	Met	Ala	Asn	Met
625					630					635					640
Ala	Ala	Cys	Ala	Ala	Ala	Cys	Ile	Arg	Gln	Ser	Ala	Trp	Leu	Arg	Pro
				645					650					655	
Arg	Met	Ser	Gln	Val	Val	Arg	Ala	Leu	Glu	Gly	Glu	Val	Ala	Leu	Arg
			660				665						670		
Lys	Val	Glu	Glu	Thr	Gly	Asn	Ser	Val	Thr	Tyr	Ser	Ser	Ser	Glu	Asn
		675				680						685			
Pro	Asn	Asp	Ile	Thr	Pro	Arg	Tyr	Gly	Thr	Asn	Lys	Arg	Arg	Phe	Asp
	690					695					700				
Thr	Gly	Ser	Ser	Asp	Gly	Tyr	Thr	Ser	Glu	Tyr	Gly	Val	Asn	Pro	Ser
705					710					715					720
Gln	Ser	Ser	Ser	Glu	His	Gln	Gln	Val	Asn	Thr					
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<213> Artificial Sequence

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<220>

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N(7) =A/g

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27

<210> 19

<211> 9

<212> PRT

<213> Brassica napus

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> X(1) =F/Y

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1 5

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

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=A/g N(8) =T/c

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aanatncnng ccatnccnaa nn

22

<210> 21

<211> 8

<212> PRT

<213> Brassica napus

<400> 21

Asp Phe Gly Met Ala Arg Ile Phe
1 5

<210> 22

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

taaccaacaa gagaca

16

<210> 23

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>
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 =A/g N(8) =I N(9) =A/g N(10) =A/g

<400> 23
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<210> 24
 <211> 8
 <212> PRT
 <213> Arabidopsis thaliana

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 1 5

<210> 25
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 <223> Description of Artificial Sequence: primer

<400> 25
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70	80	90	100	110	120
CATTTGCCTT	TTTGATTAG	ATCCAAAGAA	GCAGACAIGT	CCTCGGCGCC	GTCTCCGGGG
130	140	150	160	170	180
ACTGGTTGCG	CTCCATCTCC	ACCATCAAAC	TCCACAACCA	CCACTCCTCC	TCCAGCTTCC
190	200	210	220	230	240
GCTCCTCCTC	CCACCACACC	TTCTTCTCCT	CCGCCGCCAT	CCACTATTCC	GACATCTCCT
250	260	270	280	290	300
CCTCCTTCTT	CTCGCTCTAC	ACCTTCTGCT	CCTCCTCCAT	CTCCACCAAC	TCCATCTACG
310	320	330	340	350	360
CCGGGATCTC	CACCTCCTCT	TCCTCAGCCG	TCTCCACCCG	CTCCAACCTAC	GCCCGGATCT
370	380	390	400	410	420
CCACCCGCAC	CTGTACTTCC	TCCTACTCGA	AACCCTCCAC	CTTCAGTCCC	AGGACCACCG
430	440	450	460	470	480
TCCAATCCTT	CACGCGAAGG	AGGATCTCCT	CGACCTCCAT	CTTCTCCCTC	GCCGCCGTCT
490	500	510	520	530	540
CCTTCTTCCG	ACGGTTTATC	AACAGGAGTG	GTGGTGGGAA	TCGCCATCGG	AGGAGTCGCT
550	560	570	580	590	600
CTGCTTGTA	TAGTGACTCT	GATTTGTCTC	CTCTGTAAGA	AGAAACGACG	GAGAGACGAA
610	620	630	640	650	660
GAAGATGCTT	ACTATGTTCC	TCCGCCACCT	CCTCCTGGTC	CCAAAGCCGG	AGGACCTTAC
670	680	690	700	710	720
GGTGGACAGC	AGCAACAATG	GCGGCAACAA	AACGCAACAC	CACCGTCAGA	TCATGTCGTG
730	740	750	760	770	780
ACGTCACTAC	CACCACCACC	TAAGGCTCCA	TCTCCACCAC	GGCAACCTCC	TCCACCTCCA
790	800	810	820	830	840
CCACCGCCTT	TCATGAGCAG	CAGCGGCGGC	TCCGACTACT	CGGACCGTCC	AGTTCTTCCT
850	860	870	880	890	900
CCACCGTCTC	CAGGGCTTGT	GTTAGGCTTC	TCCAAAAGCA	CTTTCACATA	CGAGGAGCTA
910	920	930	940	950	960
GCTAGAGCCA	CCAATGGTTT	CTCCGAGGCG	AACTTGTTAG	GACAAGGCGG	GTTCGGTTAC
970	980	990	1000	1010	1020
GTGCACAAAG	GTGTGTTGCC	TAGTGGGAAA	GAAGTTGCTG	TGAAGCAGTT	GAAAGTTGGG
1030	1040	1050	1060	1070	1080
AGTGGTCAGG	GAGAGAGGGA	GTTTCAGGCA	GAGGTTGAGA	TCATCAGCAG	AGTTCACCAC
1090	1100	1110	1120	1130	1140
AGGCATCTGG	TGTCTCTTGT	TGGTTATTGC	ATCGCCGGTG	CCAAAAGATT	GCTTGTCTAT
1150	1160	1170	1180	1190	1200
GAGTTTGTTT	CTAACACAA	TCTCGAGCTT	CACCTCCATG	GCGAGGGACG	GCCTACAATG
1210	1220	1230	1240	1250	1260
GAATGGAGCA	CCAGATTGAA	GATTGCTCTT	GGATCTGCTA	AAGGACTTTC	TTATCTTCAT
1270	1280	1290	1300	1310	1320
GAAGATTGCA	ATCCTAAAAT	CATTACCCGT	GATATCAAGG	CTTCAACAT	ATTGATAGAT
1330	1340	1350	1360	1370	1380
TTCAAGTTTG	AAGCTAAGGT	TGCTGATTTT	GGTCTTGCTA	AGATTGCTTC	TGATACAAAC
1390	1400	1410	1420	1430	1440
ACGCATGTAT	CAACACGTGT	GATGGGAACC	TTTGGGTACT	TGGCTCCGGA	ATACGCTGCA
1450	1460	1470	1480	1490	1500
AGCGGAAAGC	TCACGGAGAA	GTCTGACGTT	TTCTCATTTG	GCGTTGTGCT	TTTGGAGCTC
1510	1520	1530	1540	1550	1560

Figure 1(d) (continued on next page)